

AMENDMENTS TO THE CLAIMS

1-23. (Cancelled)

24. (Amended) A method for creating a metabolic network representing metabolic reactions that take place in an organism, comprising:

providing a table of reactants and products from metabolic reactions known to take place in an organism;

selecting a nucleic acid sequence corresponding to a gene of unknown function in said organism; and

determining whether said nucleic acid sequence corresponds to a metabolic gene in said organism, based on the homology of the nucleic acid sequence to metabolic genes of other organisms,

wherein if the nucleic acid sequence corresponds to a known [is known to be a] metabolic gene, then reactants, products and stoichiometry of a reaction involving [from] a gene product of said metabolic gene are added to the table of reactants and products to create a metabolic network for said organism.

25. (Previously Presented) The method of Claim 24, wherein determining whether said nucleic acid sequence corresponds to a metabolic gene comprises determining whether said gene product corresponds to a gene product involved in cellular metabolism.

26. (Previously Presented) The method of Claim 25, wherein determining whether said nucleic acid sequence corresponds to a gene involved in cellular metabolism comprises determining whether said gene product corresponds to a gene product selected from the group consisting of: a central metabolism gene product, an amino acid metabolism gene product, a nucleotide metabolism gene product, a fatty acid metabolism gene product, a lipid metabolism gene product, a carbohydrate assimilation gene product, a vitamin biosynthesis gene product, a cofactor biosynthesis gene product, an energy generation gene product and a redox generation gene product.

27. (Previously Presented) The method of Claim 24, wherein said method is performed by a computer.

28. (Previously Presented) The method of Claim 24, further comprising applying constraints on said metabolic network that reflect the metabolic requirements of said organism.

29. (Previously Presented) The method of Claim 28, further comprising performing a flux balance analysis of said metabolic network to infer whether said organism can survive under said constraints.

30. (Previously Presented) The method of Claim 28, wherein said constraints represent the minimal media composition required to sustain growth of the organism.

31. (Previously Presented) The method of Claim 28, wherein said constraints represent the optimal requirements for maximizing growth of the organism.

32. (Previously Presented) The method of Claim 24, wherein said metabolic network is represented by a stoichiometric matrix.

33. (Previously Presented) A system for providing a metabolic network representing metabolic reactions that take place in an organism, comprising:

a table of reactants and products from metabolic reactions known to take place in an organism;

a first process for determining reactants, products and stoichiometry of a metabolic reaction from a gene product encoded by a gene of unknown function in said organism; and

a second process for determining whether said gene corresponds to a metabolic gene in said organism, based on the homology of the gene to metabolic genes of other organisms,

wherein if the gene is found to be a metabolic gene, then the reactants, products and stoichiometry of said gene product are added to the table of reactants and products to create a system for representing the reactions that take place in said organism.

34. (Previously Presented) The system of Claim 33, wherein determining whether said gene corresponds to a metabolic gene comprises determining whether said gene product corresponds to a gene product involved in cellular metabolism.

35. (Previously Presented) The system of Claim 34, wherein determining whether said gene corresponds to a gene involved in cellular metabolism comprises determining

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whether said gene product is selected from the group consisting of: a central metabolism gene product, an amino acid metabolism gene product, a nucleotide metabolism gene product, a fatty acid metabolism gene product, a lipid metabolism gene product, a carbohydrate assimilation gene product, a vitamin biosynthesis gene product, a cofactor biosynthesis gene product, an energy generation gene product and a redox generation gene product.

36. (Previously Presented) The system of Claim 33, wherein said method is performed by a computer.

37. (Previously Presented) The system of Claim 33, further comprising applying constraints on said metabolic network that reflect the metabolic requirements of said organism.

38. (Previously Presented) The system of Claim 37, further comprising performing a flux balance analysis of said metabolic network to infer whether said organism can survive under said constraints.

39. (Previously Presented) The system of Claim 37, wherein said constraints represent the minimal media composition required to sustain growth of the organism.

40. (Previously Presented) The system of Claim 33, wherein said constraints represent the optimal requirements for maximizing growth of the organism.

41. (Previously Presented) A system for representing metabolic reactions that take place in an organism, comprising:

a metabolic network comprising a table of reactants and products representing metabolic reactions that take place in an organism, wherein at least one of the metabolic reactions were determined by a process comprising:

determining a gene that encodes a gene product of unknown function in said organism; and

determining whether said gene corresponds to a metabolic gene in said organism, based on the homology of the gene to metabolic genes of other organisms,

wherein if the gene is found to be a metabolic gene, then reactants, products and stoichiometry from metabolic reactions of said gene product are added to the table of reactants and products.

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42. (Previously Presented) The system of Claim 41, wherein determining whether said gene corresponds to a metabolic gene comprises determining whether said gene encodes a gene product involved in cellular metabolism.

43. (Previously Presented) The system of Claim 42, wherein determining whether said gene corresponds to a gene involved in cellular metabolism comprises determining whether said gene encodes a gene product selected from the group consisting of: a central metabolism gene product, an amino acid metabolism gene product, a nucleotide metabolism gene product, a fatty acid metabolism gene product, a lipid metabolism gene product, a carbohydrate assimilation gene product, a vitamin biosynthesis gene product, a cofactor biosynthesis gene product, an energy generation gene product and a redox generation gene product.

44. (Previously Presented) The system of Claim 41, wherein said method is performed by a computer.

45. (Previously Presented) The system of Claim 41, further comprising applying constraints on said metabolic network that reflect the metabolic requirements of said organism.

46. (Previously Presented) The system of Claim 45, further comprising performing a flux balance analysis of said metabolic network to infer whether said organism can survive under said constraints.

47. (Previously Presented) The system of Claim 45, wherein said constraints represent the minimal media composition required to sustain growth of the organism.

48. (Previously Presented) The system of Claim 41, wherein said constraints represent the optimal requirements for maximizing growth of the organism.